

# 2025

[illegible]

387	396	405	414	423	432
GAA GCT GCA GAG GGT GAC GGT GAT AAG AAG GGG AAT GCA GAG GGC AGC AGC GAC					
E A A E G D G D K K G N A E G S S D					
441	450	459	468	477	486
GAG GAA GGG AAG CTG GTC ATT GAT GAG CCA GCC AAG GAG AAG AAC GAG AAA GGA					
E E G K L V I D E P A K E K N E K G					
495	504	513	522	531	540
GCG TTG AAG AGG AGA GCA GGG GAC TTG CTG GAG GAC TCT CCT AAA CGT CCC AAG					
A L K R A G D L L E D S P K R P K					
549	558	567	576	585	594
GAG GCA GAA AAC CCT GAA GGA GAG AAG GAG GCA GCC ACC TTG GAG GTT GAG					
E A E N P E G E K E A A T L E V E					
603	612	621	630	639	648
AGG CCC CTT CCT ATG GAG GTG GAA AAG AAT AGC ACC CCC TCT GAG CCC GGC TCT					
R P L P M E V E K N S T P S E P G S					
657	666	675	684	693	702
GGC CGG GGG CCT CCC CNN NNN NNN NNN NNN NNN NNN NNN NAG GAA GAG GCT					
G R G P P P X X X X X X X X X X X E E A					
711	720	729	738	747	756
ACC AAG GAA GAT GCT GAG GCC CCA GGC ATC AAG AGT CAT GAG AGC CTG TAG CCA					
T K E D A E A P G I K S H E S L					

FIGURE 1B

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765	774	783	792	801	810
CCA ATG TTT CAA GAG GAG CCC CCA CCC TGT TCC TGC TGC TGT CTG GGT GCT ACT					
819	828	837	846	855	864
GGG GAA ACT GGC CAT GGG CTG CAA ACT GGG NAC CCC TTT TCC ANC NCA ANC TGN					

TNT TCT T 3'

FIGURE 1C

1 M P H A - - - - F K P G D L V F A K M K G Y P H W P A R I D D I A D G A V K P 876242  
1 M S R S N R Q K E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S G I 598956  
1 M S R S N R Q K E Y K C G D L V F A K M K G Y P H W P A R I D E M P E A A V K S G I 945419  
36 P P N K Y P I F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K 876242  
41 T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K G I 598956  
41 T A N K Y Q V F F F G T H E T A F L G P K D L F P Y E E S K E K F G K P N K R K G I 945419  
76 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E P E A A E 876242  
81 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C V E E P E P E P E A A E G I 598956  
81 G F S E G L W E I E N N P T V K A S G Y Q S S Q K K S C A A E P E V E P E A H E G I 945419  
116 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D 876242  
121 G D G D K K G N A E G S S D E E G K L V I D E P A K E K N E K G A L K R R A G D G I 598956  
121 G D G D K K G S A E G S S D E E G K L V I D E P A K E K N E K G T L K R R A G D G I 945419  
156 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T 876242  
161 L L E D S P K R P K E A E N P E G E E K E A A T L E V E R P L P M E V E K N S T G I 598956  
161 V L E D S P K R P K E S G D H E E D K E I A A L E G E R H L P V E V E K N S T G I 945419  
196 P S E P G S G R G P P X X X X X X X X E E A T K E D A E A P G I K S H E S L 876242  
201 P S E P G S G R G P P Q E E E E E E D E E E A T K E D A E A P G I R D H E S L G I 598956  
201 P S E P D S G Q G P P A E E E E G E - - - E E A A K E E A E A P G V R D H E S L G I 945419

FIGURE 2

1 CCGCTGCAAGCCGCTTTCTGCGGCTGGCCCTCTCGCCGTC n876242  
 1 ATGTCGCA-----TCAACCAGC g598956  
 41 AGCATGCCACAAGCCCTTCAAGCCCGGGGACTTGGTGTTCG n876242  
 20 AGAAGCA-GTAC--AAATGCGGGACCTGGTGTTCG g598956  
 81 CTAAGATGAAGGGCTACCTCACTGGCCCTGCCAGGATCGA n876242  
 53 CCAAGATGAAGGGCTACCACTGGCCGCCGGAATTGA g598956  
 121 CGACATCGCGGATGGCGCGCTGTAAGCCCCCAACCAACAAG n876242  
 93 CGAATGCTGCTGCTGGCTGAATACTCAACCAACAAG g598956  
 161 TACCCCAATCTTTTCTTGGCAACAACAAGCCCTTC n876242  
 133 TACCAAGTCTTTTCTGGGACCAACAAGCCCTTC g598956  
 201 TGGGCCCCCAAGACCTCTTCCCTTACGAGGAATCCAAAGA n876242  
 173 TGGGCCCAAGACCTCTTCCCTTACGAGGAATCCAAAGA g598956  
 241 GAAAGTTTGGCAAGCCCAACAAGAGGAAGGGTTTCAGCGAG n876242  
 213 GAAAGTTTGGCAAGCCCAACAAGAGGAAGGGTTTCAGCGAG g598956  
 281 GGGCTGTGGGAGATCGAGAACACCTACTGTCAAGGCTT n876242  
 253 GGGCTGTGGGAGATCGAGAACACCTACTGTCAAGGCTT g598956  
 321 CCGGCTATCAGTCTCCAGAAAGAGCTGTGTGGAAGA n876242  
 293 CCGGCTATCAGTCTCCAGAAAGAGCTGTGTGGAAGA g598956

FIGURE 3A

361 G C C T G A A C C A G A G C C C G A A G C T G C A G A G G G T G A C G G T G A T n876242  
 333 G C C T G A A C C A G A G C C C G A A G C T G C A G A G G G T G A C G G T G A T g598956  
 401 A A G A A G G G G A A T G C A G A G G G C A G C A G C G A C G A G G A A G G G A n876242  
 373 A A G A A G G G G A A T G C A G A G G G C A G C A G C G A C G A G G A A G G G A g598956  
 441 A G C T G G T C A T T G A T G A G C C A G C C A A G G A G A A C G A G A A n876242  
 413 A G C T G G T C A T T G A T G A G C C A G C C A A G G A G A A C G A G A A g598956  
 481 A G G A G C G T T G A A G A G G A G A G C A G G G G A C T T G C T G G A G G A C n876242  
 453 A G G A G C G T T G A A G A G G A G A G C A G G G G A C T T G C T G G A G G A C g598956  
 521 T C T C C T A A A C G T C C C A A G G A G G C A G A A A C C C T G A A G G A G n876242  
 493 T C T C C T A A A C G T C C C A A G G A G G C A G A A A C C C T G A A G G A G g598956  
 561 A G G A G A A G G A G G C A G C C A C C T T G G A G G T T G A G A G G C C C C T n876242  
 533 A G G A G A A G G A G G C A G C C A C C T T G G A G G T T G A G A G G C C C C T g598956  
 601 T C C T A T G G A G G T G G A A A A G A A T A G C A C C C C C T C T G A G C C C n876242  
 573 T C C T A T G G A G G T G G A A A A G A A T A G C A C C C C C T C T G A G C C C g598956  
 641 G G C T C T G G C C G G G G G C C T C C C C N N N N N N N N N N N N N N N N n876242  
 613 G G C T C T G G C C G G G G G C C T C C C C A A G A G G A A G A A G A G G G g598956

FIGURE 3B

681 NNNNNNNNAGGAAGAGGCTACCAAGGAAGATGCTGAGGC n876242  
 653 AGGATGAAGAGGAAGAGGCTACCAAGGAAGATGCTGAGGC g598956  
 721 CCCAGGCATCAAGAGTCAAGAGCCCTGTAGCCACCAATG n876242  
 693 CCCAGGCATCAGAGATCAAGAGCCCTGTAG g598956  
 761 TTTCAAGAGGAGCCCCCACCTGTTCCTGCTGCTGTGG n876242  
 723 g598956  
 801 GTGCTACTGGGGGAAACTGGCCATGGGCTGCACCTGGGNA n876242  
 723 g598956  
 841 CCCCCTTTTCCANCNCANCTGNTNTCTT n876242  
 723 g598956

FIGURE 3C

FIGURE 4A



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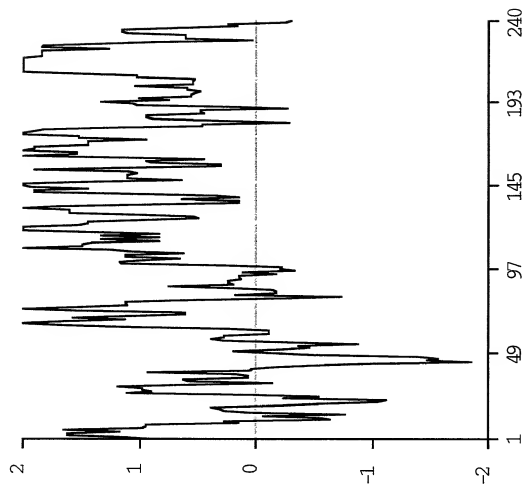


FIGURE 4B

Library	Lib Description	Abun	Pct Abun
HNT3AZT01	hNT2 cell line, teratocarcinoma, treated AZ	5	0.3425
THP1PLB02	THP-1 promonocyte cell line, treated PMA, LPS	4	0.1630
THP1PBB01	THP-1 promonocyte cell line, treated PMA	3	0.1463
PANCDIT03	pancreas, NIDDM, 57 M	1	0.1462
THP1T7T01	THP1 cells, untreated	3	0.1447
BSTMOT01	brain stem, 72 M	1	0.1214
PROSTUT12	prostate tumor, 65 M, match to PROSNOT20	4	0.1118
HUVESEP01	HUVEC endothelial cell line, shear stress	3	0.1078
PENITUT01	penis tumor, carcinoma, 64 M	4	0.1066
AMLBNOT01	AML blast cells, blast crisis, 58 F	1	0.1058
COLNNOT13	colon, ascending, 28 M	3	0.0932
HUVENOB01	HUVEC endothelial cell line, control	2	0.0841
UTRSNOT05	uterus, 45 F	3	0.0834
SINTNOT13	small intestine, ileum, ulcerative colitis, 25 F	3	0.0826
LUNGTVT03	lung tumor, 69 M, match to LUNGNOT15	5	0.0796
OVARNOM01	ovary, 49 F, WM	1	0.0752
PLACNOM02	placenta, neonatal F, NORM, WM	13	0.0722
PROSNOT01	prostate, 78 M	2	0.0702
SPLNFEM01	spleen, fetal, WM	2	0.0663
COLNNOT19	large intestine, cecum, 18 F	2	0.0585
PROSTUT05	prostate tumor, 69 M, match to PROSNOT07	4	0.0580
COLNFET02	colon, fetal F	4	0.0571

FIGURE 5A

THP1NOT01	THP1 cells, untreated	1	0.0571
LUNGNOT02	lung tumor, metastasis, 79 M, match to LUNGNOT03	3	0.0567
SININOT01	small intestine, ileum, 4 F	2	0.0560
THP1AZT01	THP-1 promonocyte cell line, treated AZ	1	0.0554
LUNGNOT15	lung, 69 M, match to LUNGNOT03	2	0.0553
LIVRFET02	liver, fetal F	2	0.0550
KERANOT02	keratinocytes, primary cell line, 30 F	3	0.0546
PROSTUT09	prostate tumor, 66 M	2	0.0529
LEUKNOT03	white blood cells, 27 F	2	0.0523
TESTNOT03	testis, 37 M	4	0.0515
COLNPOT01	colon polyp, 40 F	2	0.0513
PROSNOT14	prostate, 60 M, match to PROSTUT08	2	0.0512
BRAITUT02	brain tumor, metastasis, 58 M	3	0.0509
BRSTTUT03	breast tumor, 58 F, match to BRSTNOT05	5	0.0493
TESTNOT01	testis, 37 M	1	0.0478
UCMCNOT02	mononuclear cells	2	0.0471
THP1PLB01	THP-1 promonocyte cell line, treated PMA, LPS	1	0.0452
BRSTNOT02	breast, 55 F, match to BRSTTUT01	4	0.0443
PROSNOT02	prostate, 50 M, match to PROSTUT01	1	0.0435
COLNNOT08	colon, 60 M	1	0.0426
PANCTUT02	pancreatic tumor, carcinoma, 45 F	2	0.0403
SCORNOT01	spinal cord, 71 M	2	0.0402
UTRSNOT01	uterus, 59 F	1	0.0394
SINTTUT01	small intestine tumor, ileum, 42 M	1	0.0382

FIGURE 5B

TYLMNOR01	lymphocytes (non-adher PBMC), 24 M, RP	1	0.0379
HNT2RAT01	hNT2 cell line, teratocarcinoma, treated RA	2	0.0376
BRAINOT03	brain, 26 M	2	0.0371
LUNGNOT04	lung, 2 M	2	0.0366
PROSNOT20	prostate, 65 M, match to PROSTUT12	1	0.0336
CARDFEM01	heart, fetal, NORM, WM	3	0.0335
OVARUT01	ovarian tumor, 43 F, match to OVARNOT03	1	0.0323
OVARNOT02	ovary, 59 F	1	0.0316
NEUTGMT01	granulocytes, periph blood, M/F, treated GM-CSF	2	0.0313
BRSTNOT05	breast, 58 F, match to BRSTTUT03	2	0.0309
STOMNOT02	stomach, 52 M, match to STOMTUT01	1	0.0308
BRSTNOT07	breast, 43 F	1	0.0307
STOMNOT01	stomach, 55 M	1	0.0303
LUNGNOT18	lung, 66 F	1	0.0298
TONGTUT01	tongue tumor, carcinoma, 36 M	1	0.0295
BRAITUT08	brain tumor, astrocytoma, 47 M	2	0.0293
COLNTUT06	large intestine, cecal tumor, 45 F	1	0.0293
LIVSFEM02	liver/spleen, fetal M, NORM, WM	11	0.0290
BEPINOT01	bronchial epithelium, primary cell line, 54 M	2	0.0289
PANCNOT07	pancreas, fetal M	1	0.0287
UTRSNOT06	uterus, myometrium, 50 F	1	0.0282
LUNGNOT12	lung, 78 M	1	0.0278
TESTTUT02	testicular tumor, 31 M	1	0.0278

FIGURE 5C

THYRTUT03	thyroid tumor, benign, 17 M	1	0.0276
LATRTUT02	heart tumor, myoma, 43 M	2	0.0275
BEFINOM01	bronchial epithelium, 1° cell line, 54 M, NORM	1	0.0274
OVARNOT07	ovary, 28 F	1	0.0269
PTHYTUM01	parathyroid tumor, adenoma, M/F, NORM, WM	1	0.0268
KIDNTUT01	kidney tumor, Wilms, 8m F	1	0.0267
LATRNOT01	heart, left atrium, 51 F	1	0.0266
PROSTUT08	prostate tumor, 60 M, match to PROSNOT14	1	0.0266
BRSTNOM01	breast, F, NORM, WM	1	0.0264
BRAITUT13	brain tumor, meningioma, 68 M	1	0.0262
DUODNOT02	small intestine, duodenum, 8 F	1	0.0262
URETTUT01	ureter tumor, 69 M	1	0.0262
BRAITUT07	brain tumor, left frontal, 32 M	1	0.0259
LIVRTUT01	liver tumor, metastasis, 51 F	1	0.0259
PROSNOT18	prostate, 58 M	1	0.0256
PANCNOT08	pancreas, 65 F, match to PANCUTUT01	1	0.0254
BLADTUT04	bladder tumor, 60 M, match to BLADNOT05	2	0.0253
PLACNOB01	placenta, neonatal F	1	0.0251
LUNGNOT02	lung, 47 M	1	0.0246
TMLR3DT02	lymphocytes (non-adher PEMNC), M/F, 72-hr MLR	1	0.0246
HIPONOT01	brain, hippocampus, 72 F	1	0.0239
RATRNOT02	heart, right atrium, 39 M	1	0.0237
MMLR1DT01	macrophages (adher PEMNC), M/F, 24-hr MLR	1	0.0236

FIGURE 5D

TMRL3DT01	lymphocytes (non-adher PBMC), M, 96-hr MLR	1	0.0229
PROSN0T06	prostate, 57 M, match to PROSTUT04	2	0.0228
LIVRNOT01	liver, 49 M	1	0.0198
COLINTUT03	colon tumor, 62 M, match to COLNNOT16	1	0.0196
CRBLNOT01	brain, cerebellum, 69 M	1	0.0195
CERVNOT01	cervix, 35 F	1	0.0194
BRSTNOT04	breast, 62 F	2	0.0192
MELANOM01	melanocytes, M, NORM, WM	2	0.0192
LUNGAST01	lung, asthma, 17 M	2	0.0189
SYNOOAT01	synovium, knee, osteoarthritis, 82 F	1	0.0180
MMLR2DT01	macrophages (adher PBMC), M/F, 48-hr MLR	1	0.0178
SYNORAT04	synovium, wrist, rheumatoid, 62 F	1	0.0174
HNT2NOT01	hNT2 cell line, teratocarcinoma, control	1	0.0173
UCMCL5T01	mononuclear cells, treated IL-5	2	0.0168
CONNNOT01	fat, mesentary, 71 M	1	0.0149
BRSTTUT02	breast tumor, 54 F, match to BRSTNOT03	1	0.0140
BRAITUT01	brain tumor, oligoastrocytoma, 50 F	1	0.0134
SINTFET03	small intestine, fetal F	1	0.0130
KIDNNOT05	kidney, neonatal F	1	0.0106
CORPNOT02	brain, corpus callosum, Alzheimer's, 74 M	1	0.0103
BRSTTUT01	breast tumor, 55 F, match to BRSTNOT02	1	0.0095
LUNGFET03	lung, fetal F	1	0.0091
BRAINOM01	brain, infant F, NORM, WM	1	0.0045

FIGURE 5E